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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=18; hr=17; min=30; sec=4; ms=883;]

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Application No: 10541260 Version No: 3.0

Input Set:

Output Set:

Started: 2008-03-06 13:29:57.903
Finished: 2008-03-06 13:29:59.713
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 810 ms
Total Warnings: 104
Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

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Total Warnings: 104
Total Errors: 0
No. of SeqIDs Defined: 122
Actual SeqID Count: 122

Error code	Error Description
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SEQUENCE LISTING

<110> Watkins, Jeffry D.
Vasserot, Alain P.
Marquis , David
Huse , William D.

<120> TNF-alpha Binding Molecules

<130> X-16758M

<140> 10541260
<141> 2005-06-30

<150> PCT/US04/00290
<151> 2004-01-08

<150> 10/338,552
<151> 2003-01-08

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<170> PatentIn version 3.3

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Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser

65

70

75

80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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ccagggaaagg ggctggagtg ggttggcgaa attagatcaa aatctattaa ttctgcaaca 180

cattatgcgg agtctgtgaa agggagattc accatctcaa gagatgattc aaagaactca 240

ctgtacctgc agatgaacag cctgaaaacc gaggacacgg ccgtgtatta ctgtgctaga 300

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Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Gln Ser Val Thr Pro Lys
1 5 10 15

Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Gln Phe Val Gly Tyr Ser
20 25 30

Ile His Trp Tyr Gln Gln Lys Pro Asp Gln Ser Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Arg Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Ala
65 70 75 80

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Trp His Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

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aggttcagtg gcagtggtac tgggacagat ttcaccctca ccatcaatacg cctggaaagct 240
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Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Lys Phe Ser Asn His
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Glu Ile Arg Ser Lys Ser Met Asn Ser Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp His Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

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Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His
1 5 10

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agggccagtc agttcggtgg ctcaaggcatc cac 33

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Arg Ala Ser Gln Phe Val Gly Leu Ser Ile His
1 5 10

<210> 12
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<400> 13

Arg Ala Ser Gln Phe Val Gly Met Ser Ile His
1 5 10

<210> 14

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<400> 14

agggccagtc agttcggtgg catgagcatc cac

33

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Arg Ala Ser Gln Phe Val Gly Tyr Ser Ile His
1 5 10

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33

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1 5 10

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<400> 19

Tyr Ala Ser Glu Ser Met Ser
1 5

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tatgcttctg agtctatgtc t 21

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<400> 21

Tyr Ala Ser Glu Tyr Met Ser
1 5

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21

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1 5

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21

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<400> 25

Tyr Ala Ser Glu Ser Arg Ser
1 5

<210> 26

<211> 21

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<400> 26

tatgcttctg agtctaggc t

21

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<400> 27

Tyr Ala Ser Glu Ser Lys Ser
1 5

<210> 28

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tatgcttctg agtctaagtc t

21

<210> 29

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Tyr Ala Ser Glu Ser Xaa Ser
1 5

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21

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Tyr Ala Ser Glu Xaa Xaa Ser
1 5

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21

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Gln Gln Ser His Ser Trp His Phe Thr
1 5

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27

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1 5 10

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<400> 37

Gly Phe Lys Phe Ser Asn His Trp Met Asn
1 5 10

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Val Lys Gly

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57

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1 5 10 15

Val Lys Gly

<210> 46

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57

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Val Lys Gly

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1 5 10 15

Val Lys Gly

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Val Lys Gly

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Asn Tyr Tyr Gly Ser Thr Tyr Asp His

1 5

<210> 54

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27

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Val Lys Gly

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